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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/070,532	07/19/2002	Daniel R. Soppet	PF168P3	5548

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EXAMINER	
NICHOLS, CHRISTOPHER J	

ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 11/01/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/070,532	SOPPET ET AL.	
	Examiner	Art Unit	
	Christopher J Nichols, Ph.D.	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *17 September 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,11,13,15,17-20,22-24 and 26-47* is/are pending in the application.

4a) Of the above claim(s) *1,13,15,17-20 and 22-24* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *11 and 26-47* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) *1,11,13,15,17-20,22-24 and 26-47* are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *19 July 2002* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *9.17.04*, 9/29/04
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

1. Applicant's election with traverse of Group 4 (claims **11-12** and **16**) in the reply filed on 17 September 2004 is acknowledged. The traversal is on the ground(s) that a search of all the groups does not present a serious search burden. This is not found persuasive because the Groups as set forth in the Restriction Requirement (21 June 2004) are distinct and independent. Search and examination of all the groups presents an undue burden on the Examiner. However, as a courtesy to Applicant, three sequences will be rejoined and examined together, SEQ ID NO: 2, 4, and 6. Upon reaching allowable subject matter rejoinder of other groups will be considered. Until such time, claims **1, 13, 15, 17-20,** and **22-24** are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected inventions, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 17 September 2004. The requirement is still deemed proper and is therefore made FINAL.

Specification

2. The disclosure is objected to because of the following informalities: during scanning of the instant Application, pp. 38 became illegible. The Examiner hereby respectfully requests that the Applicant provide a copy of pp. 38 for entry into the file to ensure that a legible copy is present when the instant application passes to issue. No fault is laid on the Applicant, this error occurred due to the Office's processing of the instant application. Appropriate correction is required.

3. The disclosure is objected to because of the following informalities: typos pp. 262 line 21 "300ul" and "600ul". Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

4. Claims **11** and **26-47** are rejected under 35 U.S.C. 101 because the claimed invention is not supported by a specific, substantial, and credible asserted utility or a well-established utility.

5. The claims are directed to an isolated polypeptide comprising SEQ ID NO: 2, as well as two splice variants SEQ ID NO: 4 (splice variant 1) and SEQ ID NO: 6 (splice variant 2). The specification asserts that the polypeptide of the amino acid sequence of SEQ ID NO: 2 is a novel G-protein coupled receptor (GPCR) that shares homology and/or structural similarity to a neuropeptide receptor.

6. The art teaches that GPCRs are a gene superfamily expressed on the surface of many cell types and encompassing a massive receptor family. Gurrath (2001) "Peptide-Binding G Protein-Coupled Receptors: New Opportunities for Drug Design" Current Medicinal Chemistry **8**(13): 1605-1648 teaches that the GPCR superfamily constitutes the largest receptor family known. It is estimated that as many as 5000 distinct GFPR genes exist in the human genome. In addition, over 100 GPCRs are known with no characterized ligands and unknown physiological relevance (pp. 1606). Gurrath (2001) also teaches that all GPCRs are transmembrane receptors with a characteristic 7 transmembrane domain (TMD) motif, also known as "serpentine receptors", and all GPCRs work via a three-subunit effector system (pp. 1607; Figure 2). The state of the art holds that GPCRs fall into one of three major homology families for mammalian GPCRs: Family 1 (rho-family), Family 2 (scr-family), and Family 3 (metabotropic glutamate receptors) (pp. 1608-1609; Figure 4). Gurrath (2001) also teaches that GPCRs respond to a variety of agonists including but not limited to divalent cations, biogenic amines, fragrances, taste molecules, single amino acids, cannabinoids, prostaglandins, oligopeptides, globular proteins, chemokines, interleukins, neurotransmitters, and proteolytic enzymes (pp. 1609-1610; Table 1).

7. The specification does not disclose any data for any activity for the polypeptide of the amino acid sequence of SEQ ID NO: 2 or the splice variants, SEQ ID NO: 4 and 6. There are no working examples. There are no well-established utilities for newly discovered biological molecules. However, the specification contains several assertions of utilities, none of which are supported by data or the prior art. Therefore the claimed polypeptides lack utility as the claimed utility of a "GPCR neuropeptide receptor" while credible, is not specific or substantial.

8. The claimed utility of a "GPCR neuropeptide receptor" for the amino acid sequences of SEQ ID NO: 2, 4, and 6 is credible as they shared homology with known GPCRs.

9. The claimed utility of a "GPCR neuropeptide receptor" for the amino acid sequences of SEQ ID NO: 2, 4, and 6 is not specific because it is not clear from the specification or the claims to which GPCR is claimed, what tissues are it expressed in, and at what levels. This is of particular importance as the art recognizes a large number of GPCRs. In addition, the specification asserts that the claimed polypeptides are GPCRs, which based on its structural similarity to prior art of GPCR polypeptides that have been characterized. It is not specific because this assertion would not have been accepted by one skilled in the art because the art establishes that GPCRs, while structurally similar, are functionally diverse. The art teaches that using known and functionally established clones of GPCRs can yield genes of varying sequence homology. For instance, Howard *et al.* (2001) "Orphan G-protein-coupled receptors and natural ligand discovery." TRENDS in Pharmacological Sciences **22**(3): 132-140 teaches that the family of GPCR shares 7 TMD, and extracellular N-terminal domains, and intracellular-C-terminal domains with several conserved structural motifs. Despite this conservation of structural motifs, GPCRs usually only share ~45% sequence identity with one another. Furthermore, sequence homology is not indicative of which physiologically relevant ligands are active with a particular GPCR (pp. 132; Table 2). The assertion that SEQ ID NO: 2 (SEQ ID NO: 4 and 6) is a GPCR is not substantial because the art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases.

10. Additionally, sequence homology alone is not a reliable as the sole basis upon which to establish biological activity. For example, Skolnick and Fetrow (2000) "From gene to protein

structure and function: novel applications of computational approaches in the genomic era." Trends in Biotech. **18**(1): 34-39 state that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating the specific details of protein function (see Box 2, p. 36). Similarly, Bork (2000) "Powers and Pitfalls in Sequence Analysis: The 70% Hurdle." Genome Research **10**:398-400 states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are also echoed by Doerks *et al.* (June 1998) "Protein annotation: detective work for function prediction." Trends in Genetics **14**(6): 248-250 who state that (1) functional information is only partially annotated in the database, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity. Smith and Zhang (November 1997) "The challenges of genome sequence annotation or 'The devil is in the details'." Nature Biotechnology **15**:1222-1223 remarks that there are numerous cases in which proteins having very different functions share structural similarity due to evolution from a common ancestral gene. Brenner (April 1999) "Errors in genome annotation." Trends in Genetics **15**(4): 132-133 argues that accurate inference of function from homology must be a difficult problem since, assuming there are only about 1000 major gene superfamilies in nature, then most homologs must have different molecular and cellular functions. Finally, Bork and Bairoch (October 1996) "Go hunting in sequence databases but watch out for the traps." Trends in Genetics **12**(10): 425-427 add that the software robots that assign functions to new proteins often assign a function to a whole new protein based on

structural similarity of a small domain of the new protein to a small domain of a known protein. Such questionable interpretations are written into the sequence database and are then considered facts. In any case, the art clearly shows that structural similarity of different GPCRs is not predictive of expression patterns or functional similarity [Howard *et al.* (2001) Table 2]. Therefore, the specification's assertion that SEQ ID NO: 2 has GPCR activity is not a substantial assertion of utility, since significant further research would be required of the skilled artisan to determine what those activities are due the differences in sequence.

11. Furthermore, Sakurai *et al.* (20 February 1998) "Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior." Cell **92**(4): 573-85 (**IDS**) teaches the identification and characterization of two novel neuropeptides, orexin-A and -B, and their corresponding GPCRs. When administered to rats, these orexin-A and orexin-B stimulate food consumption. Also, prepro-orexin mRNA level is up-regulated upon fasting, suggesting a physiological role for the peptides as mediators in the central feedback mechanism that regulates feeding behavior. The GPCRs identified and characterized by Sakurai share 99.8% sequence homology with the amino acid sequence of SEQ ID NO: 2, save for one conservative amino acid substitution. Therefore the claimed polypeptides are orexin receptors involved in narcolepsy. The Specification as filed does not correctly identify the claimed polypeptides and thus is not specific.

12. The claimed utility of a "GPCR neuropeptide receptor" for the amino acid sequences of SEQ ID NO: 2, 4, and 6 is not substantial because the specification does not identify any specific ligands or GPCR functional activity. Kenakin (2002) "Drug Efficacy at G Protein-Coupled Receptors" Annu. Rev. Pharmacol. Toxicol. **42**: 349-379 teaches their binding and response to

specific ligands (agonists) is variable, as are the effects on the receptor. In addition, receptor behavior involves several reactions including but not limited to internalization, pleiotropic interaction with multiple G-proteins, desensitization, oligomerization, and interaction with membrane auxiliary proteins (pp. 357; 362-367; Figure 1-4). Further, as noted above by Gurrath (2001) and Howard *et al.* (2001) possible GPCR ligands cover a huge range of bioactive molecules including but not limited to light, Ca^{2+}, odorants, amino acids, nucleotides, peptides, fatty acid derivatives, and polypeptide ligands (pp. 132). A skilled artisan would have had to experiment significantly to identify any allergy, disease, or disorder associated with SEQ ID NO: 2. Therefore, the asserted utility is not substantial. Also as noted above, the identity of SEQ ID NO: 2 (as well as SEQ ID NO: 4 and 6) is known and not correctly identified in the Specification as filed.

13. If Applicant can submit evidence (in the form of a declaration under 37 CFR 1.132 or post-filing date publications) supporting the specification's assertion that SEQ ID NO: 2 has a specific function similar to a known G-protein coupled receptor (GPCR), wherein the specific function was predicted by the specification as originally filed, such would be viewed favorably as evidence of patentable utility.

14. Therefore, in the absence of a well-established utility, and the absence of a specific, substantial and credible asserted utility, the claimed invention lacks patentable utility under 35 U.S.C. § 101.

15. Claims **11** and **26-47** are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a credible, specific and substantial asserted

utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

16. The claims are drawn very broadly to fragments, domains, mature forms of a secreted protein, variants, alleles, and species homologues of the polypeptide of SEQ ID NO: 2 as well as SEQ ID NO: 4 and 6.

17. The specification teaches that SEQ ID NO: 4 and 6 are "splice variants" of SEQ ID NO: 2, asserted to be a neuropeptide GPCR.

18. The specification fails to provide any guidance for the successful isolation, characterization, cloning, mutation, or identification of any fragments, domains, mature forms of a secreted protein, variants, alleles, and species homologues of the polypeptide of SEQ ID NO: 2 as well as SEQ ID NO: 4 and 6. Since resolution of the various complications in regards to isolating and characterizing fragments, domains, mature forms of a secreted protein, variants, alleles, and species homologues of the polypeptide of SEQ ID NO: 2 as well as SEQ ID NO: 4 and 6 is highly unpredictable, one of skill in the art would have been unable to practice the invention without engaging in undue trial and error experimentation. In order to practice the invention using the specification and the state of the art as outlined below, the quantity of experimentation required to practice the invention as claimed would require the *de novo* determination of formulations fragments, domains, mature forms of a secreted protein, variants, alleles, and species homologues of the polypeptide of SEQ ID NO: 2 as well as SEQ ID NO: 4 and 6 followed by extensive experimentation to characterize them all. In the absence of any guidance from the specification, the amount of experimentation would be undue, and one would have been unable to practice the invention over the scope claimed. This is especially difficult as

the Specification does not assert a credible, specific, and substantial utility for the polypeptide of SEQ ID NO: 2.

19. Additionally, a person skilled in the art would recognize that predicting the efficacy of isolating/synthesizing fragments, domains, mature forms of a secreted protein, variants, alleles, and species homologues of the polypeptide of SEQ ID NO: 2 as well as SEQ ID NO: 4 and 6 based solely on an asserted utility which is incorrect as highly problematic (see MPEP §2164.02). Thus, although the specification prophetically considers and discloses general methodologies of isolating/synthesizing and characterizing fragments, domains, mature forms of a secreted protein, variants, alleles, and species homologues of the polypeptide of SEQ ID NO: 2 as well as SEQ ID NO: 4 and 6, such a disclosure would not be considered enabling since the state of protein biochemistry is highly unpredictable and complex. The factors listed below have been considered in the analysis of enablement [see MPEP §2164.01(a) and *In re Wands*, 858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988)]:

(A) The breadth of the claims;
(B) The nature of the invention;
(C) The state of the prior art;
(D) The level of one of ordinary skill;
(E) The level of predictability in the art;
(F) The amount of direction provided by the inventor;
(G) The existence of working examples; and
(H) The quantity of experimentation needed to make or use the invention based on the content of the disclosure.

20. The following references are cited herein to illustrate the state of the art of protein biochemistry.

21. Regarding fragments, domains, mature forms of a secreted protein, variants, alleles, and species homologues of the polypeptide of SEQ ID NO: 2 as well as SEQ ID NO: 4 and 6, the

problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex. While it is known that many amino acid substitutions are generally possible in any given protein the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of success are limited. Certain positions in the sequence are critical to the protein's structure/function relationship, e.g. such as various sites or regions directly involved in binding, activity and in providing the correct three-dimensional spatial orientation of binding and active sites. These or other regions may also be critical determinants of antigenicity. These regions can tolerate only relatively conservative substitutions or no substitutions [see Wells (18 September 1990) "Additivity of Mutational Effects in Proteins." Biochemistry **29**(37): 8509-8517; Ngo *et al.* (2 March 1995) "The Protein Folding Problem and Tertiary Structure Prediction, Chapter 14: Computational Complexity Protein Structure Prediction, and the Levinthal Paradox" pp. 433-506]. However, Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one of ordinary skill in the art to determine, without undue experimentation, the positions in the protein which are tolerant to change (e.g. such as by amino acid substitutions or deletions), and the nature and extent of changes that can be made in these positions. Although the specification outlines art-recognized procedures for producing and screening for active muteins, this is not adequate guidance as to the nature of active derivatives that may be constructed, but is merely an invitation to the artisan to use the current invention as a starting point for further experimentation. Even if an active or binding site were identified in the specification, they may not be sufficient, as the ordinary artisan would immediately recognize that an active or binding site must assume the proper three-

dimensional configuration to be active, which conformation is dependent upon surrounding residues; therefore substitution of non-essential residues can often destroy activity. The art recognizes that function cannot be predicted from structure alone [Bork (2000) "Powers and Pitfalls in Sequence Analysis: The 70% Hurdle." Genome Research **10**:398-400; Skolnick and Fetrow (2000) "From gene to protein structure and function: novel applications of computational approaches in the genomic era." Trends in Biotech. **18**(1): 34-39, especially p. 36 at Box 2; Doerks *et al.* (June 1998) "Protein annotation: detective work for function prediction." Trends in Genetics **14**(6): 248-250; Smith and Zhang (November 1997) "The challenges of genome sequence annotation or 'The devil is in the details'." Nature Biotechnology **15**:1222-1223; Brenner (April 1999) "Errors in genome annotation." Trends in Genetics **15**(4): 132-133; Bork and Bairoch (October 1996) "Go hunting in sequence databases but watch out for the traps." Trends in Genetics **12**(10): 425-427]. Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims and possibly screen same for activity, the lack of direction/guidance presented in the specification regarding which structural features are required in order to provide activity, the absence of working examples directed to same, the complex nature of the invention, the state of the prior art which establishes the unpredictability of the effects of mutation on protein structure and function, and the breadth of the claims which fail to recite any structural or functional limitations, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

22. Thus the specification of the instant application fails to provide adequate guidance for one of skill in the art to overcome the unpredictability and challenges as exemplified in the references herein.

23. Claims **38-47** are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

24. The claims are drawn to polypeptides having at least 95% sequence identity with a particular disclosed sequence. The claims do not require that the polypeptide possess any particular conserved structure, or other distinguishing feature, such as a specific biological activity. Thus, the claims are drawn to a genus of polypeptides that is defined by sequence identity.

25. To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim that is sufficiently disclosed is a partial structure in the form of a recitation of percent identity. The specification does not identify any particular portion of the structure that must be conserved, nor does it provide a disclosure of structure/function correlation. The distinguishing characteristics of the claimed genus are not described. The only adequately described species is

a polypeptide comprising SEQ ID NO: 2 (SEQ ID NO: 4 and 6). No active variants are disclosed. Accordingly, the specification does not provide adequate written description of the claimed genus.

26. *Vas-Cath Inc. v. Mahurkar*, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

27. One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

28. Therefore, only isolated polypeptides comprising the amino acid sequence set forth in SEQ ID NO: 2, 4, and 6, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear

that the written description provision of 35 U.S.C. §112 is severable from its enablement provision.

29. Claims **11, 32, 33, 34, 35, 36,** and **37** are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

30. The invention appears to employ novel polypeptide (i.e. the amino acid sequences of SEQ ID NO: 2, 4, and/or 6). Since the polypeptides are essential to the claimed invention they must be obtainable by a repeatable method set forth in the specification or otherwise readily available to the public.

31. The specification does not disclose a repeatable process to obtain the polypeptides and it is not apparent if the polypeptides are readily available to the public. If the polypeptides are not so obtainable or available, the requirements of 35 U.S.C. § 112 may be satisfied by a deposit of the polypeptides.

32. It is noted that Applicant has deposited the polypeptides (p. 9 of the specification), but there is no indication in the specification as to public availability. If the deposit is made under the Budapest Treaty, then an affidavit or declaration by Applicant, or a statement by an attorney of record over his or her signature and registration number, stating that the specific polypeptides have been deposited under the Budapest Treaty and that the polypeptides will be irrevocably and without restriction or condition released to the public upon the issuance of a patent, would satisfy the deposit requirement made herein. Applicant may provide assurance of compliance by an

affidavit or declaration, or by a statement by an attorney of record over his or her signature and registration number, showing that:

(a) during the pendency of this application, access to the invention will be afforded to the Commissioner upon request;

(b) all restrictions upon availability to the public will be irrevocably removed upon granting of the patent;

(c) the deposit will be maintained in a public depository for a period of 30 years or 5 years after the last request or for the effective life of the patent, whichever is longer;

(d) a test of the viability of the biological material at the time of deposit will be made (see 37 C.F.R. § 1.807); and

(e) the deposit will be replaced if it should ever become inviable.

33. Applicant's attention is directed to M.P.E.P. §2400 in general, and specifically to §2411.05, as well as to 37 C.F.R. § 1.809(d), wherein it is set forth that "the specification shall contain the accession number for the deposit, the date of the deposit, the name and address of the depository, and a description of the deposited material sufficient to specifically identify it and to permit examination." At pp. 9, the date of the deposit are missing. The specification should be amended to include such, however, Applicant is cautioned to avoid the entry of new matter into the specification by adding any other information. Finally, Applicant is advised that the address for the ATCC has recently changed, and that the new address should appear in the specification. The new address is:

American Type Culture Collection
10801 University Boulevard
Manassas, VA 20110-2209

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

34. Claim **11** is rejected under 35 U.S.C. 102(b) and 102(e) as being anticipated by US 5,935,814 (10 August 1999) Bergsma & Ellis.

35. US '814 teaches sequences that ~80% homology with SEQ ID NO: 2 (SEQ ID NO: 2 therein), 96.8% with SEQ ID NO: 4 (SEQ ID NO: 2 therein), and 99.8% with SEQ ID NO: 6 (SEQ ID NO: 2 therein) thus meeting the limitations of claim 11 for a fragment, domain, epitope, mature form, variant, allelic variant, and species homologue (Col. 4-6).

36. Claims **11, 26, 27, 28, 29, 30, 38, 39, 40,** and **41** are rejected under 35 U.S.C. 102(a) and 102(e) as being anticipated by US 6,020,157 (1 February 2000) Bergsma & Ellis (**IDS**).

37. US '157 teaches sequences that share 9~99.8% with SEQ ID NO: 2 (SEQ ID NO: 2 therein), 96.8% with SEQ ID NO: 4 (SEQ ID NO: 2 therein), and 97.7% with SEQ ID NO: 6 (SEQ ID NO: 2 therein) thus meeting the limitations of claim 11 for a fragment, domain, epitope, mature form, variant, allelic variant, and species homologue, as well as claims 26, 38 (Col. 4-6).

38. US '157 teaches that said sequences may lack a single amino acid and may be produced via expression in a host cell thus meeting the limitations of claims 27, 30, 41 (Example 2).

39. US '157 teaches fusion proteins comprising said sequences and compositions of said sequences thus meeting the limitations of claims 28, 29, 39, 40, and 41 (Col. 6, 20-21).

40. Claims **11, 26, 27, 28, 29, 30, 31, 38, 39, 40, 41,** and **42** are rejected under 35 U.S.C. 102(e) as being anticipated by US 6,664,229 (16 December 2003) Hagan *et al.*

41. US '229 teaches sequences that share ~99.8% with SEQ ID NO: 2 (SEQ ID NO: 22 therein), ~96.8% with SEQ ID NO: 4 (SEQ ID NO: 23 therein), and 99.8% with SEQ ID NO: 6 (SEQ ID NO: 23 therein) thus meeting the limitations of claim 11 for a fragment, domain, epitope, mature form, variant, allelic variant, and species homologue, as well as claims 26, 38 (Col. 4, 10, 13-14).

42. US '229 teaches that said sequences may lack a single amino acid and may be produced via expression in a host cell thus meeting the limitations of claims 27, 30, 41 (Col. 12).

43. US '229 teaches fusion proteins comprising said sequences, glycosylated forms of said sequences, and compositions of said sequences thus meeting the limitations of claims 28, 29, 31, 39, 40, and 41 (Col. 8, 10 20).

Summary

44. No claims are allowed.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to **Christopher James Nichols, Ph.D.** whose telephone number is **(571) 272-0889**. The examiner can normally be reached on Monday through Friday, 8:00 AM to 5:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, **Brenda Brumback** can be reached on **(571) 272-0961**.

The fax number for the organization where this application or proceeding is assigned is **703-872-9306**.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see **http://pair-direct.uspto.gov**. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at **866-217-9197** (toll-free).

CJN
October 18, 2004

Elizabeth C. Kemmerer

ELIZABETH KEMMERER
PRIMARY EXAMINER